REMARKS

Claims 1-15 currently are pending. Claims 1, 2, 3, 6, 7, 11, 13 and 15 have been amended.

The examiner stated that claims 2, 3, 6, and 7 are rejected under 35 USC § 101 because the claimed invention is directed to non-statutory subject matter.

Applicants amend claims 2 and 3 as suggested by the examiner and now recited "An isolated amino acid sequence..." Applicants amend claims 6 and 7 to recited "A transformed microorganism..."

The examiner rejected claims 1, 2, and 4-15 under 35 USC § 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid encoding a nitrilase comprising the amino acid sequence of SEQ ID NO: 2 or an isolated nucleic acid of SEQ ID NO: 1 encoding a nitrilase; does not reasonably provide enablement for any other embodiment. The examiner stated that the specification does not teach the specific catalytic amino acids and the structural motifs which are essential for enzyme structure and activity/function.

Applicants respond by narrowing the scope of claim 1 by amending claim 1 to include sequences which have at least 97% homology. Applicants believe one of ordinary skill in the art could determine which sequences would retain protein function and have 97% homology. The support for the amendment is found on page 13, lines 7-11 of the instant specification.

The examiner believes claim 1 is vague because of the phrase "as a result of the degeneracy of the genetic code." Definiteness of claim language must be analyzed, not

in a vacuum, but in light of the claim interpretation that would be given by one possessing the ordinary level of skill in the pertinent art at the time the invention was made. MPEP § 2173.02. One of ordinary skill in the art knows that degeneracy of the genetic codes refers to some amino acids being encoded by more than one codon. Applicants attach page 328 of *The Dictionary of Gene Technology* to support applicants' argument.

Applicants believe the present amendment of claims 2 and 3 overcomes the examiner's indefiniteness rejections of claims 2 and 3.

The examiner stated that claim 8 is vague and indefinite because it is not known how the claimed process can prepare chiral carboxylic acids in the presence of an "amino acid sequence." Also, the examiner stated that the phrase "growing, dormant or disrupted microorganism" is vague and indefinite because the meaning of the phrase is not known.

Claims 8, as amended by the preliminary amendment of 10/13/99 does not recite "growing, dormant or disrupted microorganism."

Applicants delete "[sic]" from claims 11 and 13.

Claims 1, 3, 5, 6 and 7 are rejected as being anticipated by Kobayashi et al. because the examiner believes the reference teaches a polynucleotide sequence which encodes a nitrilase having at least 96.09% identity to SEQ ID NO: 1, vector containing said polynucleotide sequence, and bacterial host cell comprising said vector. The examiner rejected claim 2 under the same reference because he believes the reference teaches a nitrilase having at least 96.09% identity to SEQ ID NO: 2 encoded by the nucleotide

sequence Accession D13419, vector containing said polynucleotide sequence and bacterial host cell comprising said vector.

Applicants have amended claim 1 to recite 97% homology. Anticipation can only be established by a single prior art reference which discloses each and every element of the claimed invention.. *RCA Corp. v. Applied Digital Data Systems, Inc.*, 730 F.2d 1440, 1444, 221 USPQ 385, 388 (Fed. Cir. 1984). Therefore, Kobayashi et al. do not teach each and element of claim 1.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such account.

Respectfully submitted,

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COMPLETE LISTING OF CLAIMS IN THE APPLICATION

1. (currently amended) An isolated nucleic acid sequence which codes for a polypeptide having nitrilase activity, selected from the group consisting of:

   a) a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1,

   b) a nucleic acid sequences which are derived from the nucleic acid sequence depicted in SEQ ID NO: 1 as a result of the degeneracy of the genetic code,

   c) derivatives of the nucleic acid sequence depicted in SEQ ID NO: 1, which code for polypeptides having the amino acid sequences depicted in SEQ ID NO: 2 and have at least ~~95~~ 97% homology at the amino acid level, with negligible reduction in the enzymatic action of the polypeptides.

2. (currently amended) An isolated amino acid sequence encoded by a nucleic acid sequence as claimed in claim 1.

3. (currently amended) An isolated amino acid sequence as claimed in claim 2, encoded by the sequence depicted in SEQ ID NO: 1.

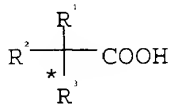
4. (original) A nucleic acid construct comprising a nucleic acid sequence as claimed in claim 1, the nucleic acid sequence being linked to one or more regulatory signals.

5. (previously presented) A vector comprising an nucleic acid sequence as claimed in claim 1.

6. (currently amended) A transformed microorganism comprising at least one nucleic acid sequence as claimed in claim 1.

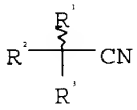
7. (currently amended) A <u>transformed</u> microorganism comprising at least one nucleic acid sequence as claimed in claim 1.

8. (previously presented) A process for preparing chiral carboxylic acids of the general formula I



(I),

which comprises converting racemic nitriles of the general formula II



(II)

in the presence of an amino acid sequence as claimed in claim 2, and where at least 25 mmol of nitrile are converted per h and per mg of protein, or 25 mmol of nitrile are converted per h and per g of dry weight, into the chiral carboxylic acids,

where the substituents and variables in the formulae I and II have the following meanings:

* an optically active center

R^1, R^2, R^3 independently of one another hydrogen, substituted or unsubstituted, branched or unbranched C_1–C_{10}-alkyl, C_2–C_{10}-alkenyl, substituted or unsubstituted aryl, hetaryl, OR^4 or NR^4R^5 and where the radicals R^1, R^2 and R^3 are always different,

R^4 hydrogen, substituted or unsubstituted, branched or unbranched C_1–C_{10}-alkyl, C_2–C_{10}-alkenyl, C_1–C_{10}-alkylcarbonyl, C_2–C_{10}-alkenylcarbonyl, aryl, arylcarbonyl, hetaryl or hetarylcarbonyl,

R^5 hydrogen, substituted or unsubstituted, branched or unbranched C_1–C_{10}-alkyl, C_2–C_{10}-alkenyl, aryl or hetaryl.

9. (original) A process as claimed in claim 8, wherein one of the substituents R^1, R^2 or R^3 is OR^4.

10. (previously presented) A process as claimed in claim 8, wherein one of the substituents R^1, R^2 or R^3 is aryl.

11. (currently amended) A process as claimed in claim 8, wherein the process is carried out in an aqueous reaction solution at a pH between 4 and ~~to [sic]~~ 11.

12. (previously presented) A process as claimed in claim 8, wherein from 0.01 to 10% by weight of nitrile or from 0.01 to 10% by weight of a corresponding aldehyde or ketone and from 0.1 to 10% by weight of hydrocyanic acid are reacted in the process.

13. (currently amended) A process as claimed in claim 8, wherein the process is carried out at a temperature between 0°C and ~~to [sic]~~ 80°C.

14. (previously presented) A process as claimed in claim 8, wherein the chiral

carboxylic acid is isolated from the reaction solution in yields of from 60 to 100% by extraction or crystallization or extraction and crystallization.

15. (currently amended) A process as claimed in claim 8, wherein the chiral carboxylic acid has an optical purity of at least 90%~~ee~~.